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- 1. Conner et al. (1983) PNAS 80: 278-282.
- 2. Rollini et al. PNAS (1985 Nov) 82(12): 7197-7201.
- 3. Gorski et al. IMMUNOGENTICS (1987) 25(6):379-402.
- 4.. de Preval et al. IMMUNOGEENTICS (1987) 26(4-5): 249-257.
- 5. Irle et al. J. EXPERIMENTAL MEDICINE (1988 Mar 1) 167(3): 853-872.

6. Andersson et al. IMMUNOGENETICS (1988) 28 (1): 1-5.

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The single DR_{β} gene of the DRw8 haplotype is closely related to the $DR_{\beta}3III$ gene encoding DRw52

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Abstract. In most individuals two HLA- DR_{β} genes are expressed from each chromosome. One of these genes encodes one of the classical DR specificities, while the other encodes either of the supertypic DRw52/DRw53 specificities. In addition to these genes usually one or two DR_{β} pseudogenes are present. In contrast, the DRw8 chromosomal region only contains a single DR_{β} gene. To determine the relationship of this single gene to the multiple DR_{β} genes of other DR specificities, comparisons of Southern genomic blots were carried out. In this analysis genomic clones for each individual DR_{β} chain locus were included. The $DR_{\beta}w8$ gene was indistinguishable from the $DR_{\beta}III$ gene of DR3 cells (encoding DRw52), suggesting that it is closely related to the latter gene. The functional implications of this finding are discussed.

Introduction

Class II histocompatibility antigens in man are encoded by the HLA-D region. Serological, cellular, and, more recently, molecular cloning analyses have shown that this region is composed of three major subregions, HLA-DR, -DQ, and -DP. From each subregion at least one class II molecule consisting of an α and a β chain is expressed (Albert et al. 1985). The class II antigens are extremely polymorphic (Bach 1985). A large number of serologically defined DR specificities are known. By the use of cellular methods several of these specificities have been further split. These specificities correspond to allelic series of DR_{β} chains, while the DR_{α} chain is invariable. Two separate allelic series of DR specificities, the classical DR and DRw52/DRw53, have been established by serological

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studies. The DR series involves a large number of alleles, while the DRw52/DRw53 polymorphism is much more restricted (reviewed in Mach et al. 1986). The DRw52 specificity is carried by DR3, 5, w6, and w8 individuals, whereas those with DR specificities 4, 7, and w9 have the DRw53 specificity. More than one DR $_{\beta}$ chain is expressed from each chromosome for most of the DR specificities (Rollini et al. 1985, Giles and Capra 1985). Epitopes corresponding to the supertypic specificities DRw52 and DRw53 are present on β chains separate from those displaying the classical DR specificities (Tanigaki and Tosi 1982).

In addition to the sequence variability between DR alleles there is a variability in the number of DR_B genes (Böhme et al. 1985). Molecular cloning and genomic hybridizations have shown that three DR_{β} genes, designated I, II, and III, are present in the DR3, 5, and w6 haplotypes (Rollini et al. 1985). $DR_{\theta}I$ encodes the DR3 specificity, DR_BIII corresponds to the DRw52 epitope (Gorski et al. 1985), while $DR_{\beta}II$ is a pseudogene. In the DR4 haplotype four DR_{θ} genes exist, two of which are pseudogenes, while the other two encode the DR4 and DRw53 specificities. Hybridization experiments have shown that the DR7 and DRw9 haplotypes have a gene organization similar to DR4 (Böhme et al. 1985, Andersson et al. 1987). These studies also indicated that the DR2 haplotype contains three and the DRI haplotype two DR_B gencs. In the DRw8 haplotype a single DR_8 gene has been found (Böhme et al. 1985). The present study was undertaken to clarify the relationship of this single gene to the multiple genes encountered in the DR3 and DR4 haplotypes. Since detailed molecular information is available from the cloned DR_H genes of the DR haplotypes DR3 and DR4 it is possible to assign every single restriction fragment hybridizing with a DR₆ probe in Southern hybridizations of restricted DNA of these haplotypes to a specific gene. To minimize allelic restriction site polymorphism which might make such a comparison impossible, we decided to use hybridization probes corresponding

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to the reasonably well-conserved 3' portions of the DR_{β} genes.

Materials and methods

DNA sources. DNA was prepared from the following homozygous typing cells that were selected from the typing panels used at the State Institute for Blood Group Serology, University Hospital, Linköping, Sweden: PH, DR1/1; IML, DR2/2; DL, DR3/3; SA, DR5/5; and IH, DR7/7.

Cell lines SPL, DRw8/w8 and KOZ, DRw9/DRw9 were obtained from Dr. J. Bodmer of the Tissue Antigen Laboratory, Imperial Cancer Research Fund Laboratories, London, England. Additional DNA was prepared from the cells used in our earlier work: BO, DR4/4 (Andersson et al. 1987) and GP, DRw6/w6 (Böhme et al. 1985).

Hybridization probes. Two DR_{β} -specific probes corresponding to (i) the cytoplasmic exon with flanking introns and (ii) the DR_{β} 3'-untranslated exon were used (Table 1). After restriction enzyme digestions of the clones, the probe fragments were isolated by preparative agarose gel electrophoresis. Fragments were radioactively labeled to high specific activity with $\alpha(-^{32}P)$ deoxycytidine triphosphate by either nick-translation (Rigby et al. 1977) or random priming (Feinberg and Vogelstein 1984).

DNA preparation and Southern blot analysis. DNA was isolated from either 5 ml of peripheral blood according to the method of Böhme and

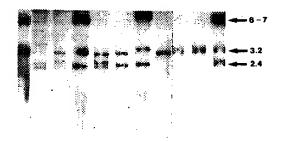
co-workers (1983) or 500 μ l of pelleted cultured cells as described by Grosveld and co-workers (1982). Samples of 10 μ g of human DNA were digested to completion with restriction enzymes according to the manufacturer's recommendations. The digests were separated by agarose gel electrophoresis in 0.7 and 1.5% gels, in 1 \times TBE (89 mM Tris-borate buffer, pH 8.3, 2.5 mM ethylenediaminetetraacetate). Southern transfer of restricted DNA to Biodyne hybridization membranes (Pall) was made overnight with 1 \times SSC (0.015 M sodium citrate buffer, pH 7.0, 0.15 M NaCl). Hybridizations were carried out in 40% formamide at 42 °C. Washings were performed at high stringency (0.2 \times SSC, 0.25% sodium dodecyl sulfate) at 58 °C for 1 h.

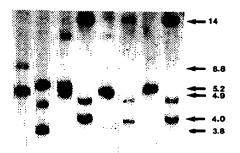
Results and Discussion

To define the relationship of the DR_{β} gene carried by DRw8 individuals to those of the DR3 and DR4 haplotypes, genomic DNA samples from homozygous typing cells of DR specificities 1 to w9 were separately digested with Pst I, Bam HI, and Hind III and hybridized to a probe corresponding to exon 5 of DR_{β} genes (Table 1). Hybridization to Hind III-digested DNA is shown in Figure 1. In all cases a single hybridizing fragment was found for the DRw8 cells, which is in agreement with the proposal that this haplotype contains only a single DR_{β} gene. A single DR_{β} fragment in DRw8 cells was also obtained when genomic DNA digested with Pvu II was

Table 1. Documentation of hybridization probes

Probe corresponding to	Type of clone	Designation of clone	Restriction sites employed	Size of probe fragment (bp)	Reference		
DR_{β} exon 5 and intron	Genomic	p801-2	Bgl II	376	Larhammar et al. 1985		
DR _g exon 6	cDNA pII-β-4		Pst I	220	Gustafsson et al. 1984		





DR 1 2 3 4 5 w6 7 w8w6w8w9

Fig. 1. Hybridization with the DR_{β} exon 5-specific probe to Hind III-restricted human genomic DNA corresponding to DR specificities 1 to w9. The sizes of restriction fragments are given in kilobases

DR 1 2 3 4 5 7 w8w9

Fig. 2. Restriction fragment patterns of human genomic DNA, representing the same individuals as in Figure 1, digested with Pvu II and hybridized with the DR_{β} 3'-untranslated probe. The sizes of restriction fragments are given in kilobases

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Table 2. C

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escribed by DNA were ling to the parated by 3E (89 mM traacetate). ation membrane out in 40% stringency for 1 h.

hybridized with the probe corresponding to the 3'-untranslated exon (Fig. 2). In all these experiments the hybridizing fragment of DRw8 cells coincided with fragments present in DR3, 5, and w6 DNA, but not with fragments in DR4, 7, and w9 DNA (Table 2). These findings suggested that the $DR_{\beta}w8$ gene is closely related to one of the genes present in the DR3, DR5, and DRw6 haplotypes.

To further investigate this possibility, cosmid clones 4-1, 6-2, and 10-4, containing the $DR_{\beta}3$ genes *I*, *II*, and *III*, respectively (Rollini et al. 1985), were run in parallel

with DR3 and DRw8 genomic DNA on agarose gels after separate digestion with Pst I, Pvu II, and Hind III. The digests were hybridized with the DR $_{\beta}$ probes used above, and the results are compiled in Table 2. A representative result obtained after Hind III digestion is shown in Figure 3. It is evident that all hybridizing fragments in the DR3 DNA can be accounted for by fragments in the three cosmids (Table 2 and Fig. 3, lanes 1-3). The DRw8 fragments coincided in all cases with fragments derived from the $DR_{\beta}3III$ gene, i.e., the gene encoding the $DR_{\beta}w52$ molecule.

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Table 2. Occurrence of bands in DNA from homozygous typing cells of different DR specificities digested with Bam HI, Hind III, Pst I, and Pvu II and hybridized with the DR_B probes from Table 1

Probe and enzyme	Size*	DR specificity								Restriction fragments corresponding to DR_B3 genes [*]	
		1	2	3	4	5	w6	7	w8	w9	sponding to tongo genes
DR _g 3'UT, Pvu II	3.8		+				ND	٢			
Σ. μ	4.0				+			+		+	
	4.5		+								
	4.6				+			+		+	
	4.9	· +		+		+					βΙ
	5.2			+					+		βIII
	5.3		+								
	6.8	+									
	11			+		+					$oldsymbol{eta}$ II
	14				+			+		+	
DR ₈ exon 5 and intron, Pst I	0.1				+			+		+	
- · · p	0.45	+	+								
	0.52		+	+	+	+	+	+		+	$oldsymbol{eta}$ II
	0.57				+			+		+	
	0.65	+									
	0.9		+								
	0.95			+		+	+		+		βIII
	1.0			+		+	+				$oldsymbol{eta}$ I
	1.1				+			+		+	
	2.0				+			+		+	
DR ₆ exon 5 and intron, Barn HI	0.3	ND	t	+	+	+	+	+		+	ND
one of the state o	0.6				+			+		+	
	0.85		+	+		+	+		+		
	10				+			+		+	
	14		+	+		+	+				
DR_{θ} exon 5 and intron, Hind III	0.5			+		+	+				βΙ
	2.2		+								
	2.3			+		+	+				βΙ
	2.4		+		+			+		+	
	2.5		•	+		+					$oldsymbol{eta}$ II
	3.0	+		+		+	+		+		βΙΙΙ
	3.2	•			+			+		+	
	3.6		+								
	6.0	+	•								
	6.5	-			+			+		+	
	7.5				+			+		+	

nic DNA, vith Pvu II of restric-

^{*} Sizes in kilobases

† ND, not done

^{*} The restriction fragments corresponding to different DR_β genes were determined by Southern blot analysis of representative cosmid clones (see text)

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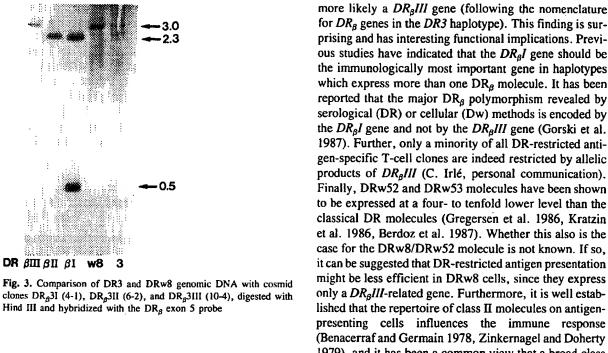
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This result clearly indicates that the DR_6w8 gene is closely related to the DR₈w52 gene and thus might be a DRw52 allele. In this respect, it is of interest that oligonucleotide probes specific for each of the three DR₈III alleles identified by DNA sequencing (DRw52a, w52b, and w52c) are negative in hybridization with DRw8 DNA, suggesting the existence of an additional DR_BIII allele (Tiercy et al. 1987). Interestingly, DRw8 cells have been reported to react with some but not all DRw52 sera (Baldwin et al. 1985). This fact and the results above suggest that the DRw8 and DRw52 epitopes are carried by the same DR_B chain. Serologically, DRw52 and DRw53 are regarded as belonging to the same allelic series (Bach 1985). This notion was recently questioned, since a comparison of the restriction maps and DNA sequences of the $DR_{\beta}w53$ gene with those of the three $DR_{\beta}3$ genes I, II, and III suggested that the DR_6w53 gene is more closely related to $DR_{\theta}3II$ than to $DR_{\theta}3III$ encoding the $DR_{\theta}w52$ chain (Gorski et al. 1987). It should be noted, however, that careful sequence analyses of the four DR_64 genes showed that extensive exchanges of sequences have occurred among these nonallelic genes, making allelic relationships difficult to establish (Andersson et al. 1987). The sequence of the DR₈w8 first domain exon was recently reported by Bell and co-workers (1987). A comparison of this sequence with those of other DR₆ first domain exons does not provide any clear answer concerning the relationship of the DR₈w8 gene. More extensive sequence information is needed to clarify this matter.

DR β III β II β I

The results of the present study suggest that the single DR_{β} gene in the DRw8 haplotype is not a $DR_{\beta}I$ gene but

for DR_B genes in the DR3 haplotype). This finding is surprising and has interesting functional implications. Previous studies have indicated that the DR₈I gene should be the immunologically most important gene in haplotypes which express more than one DR₈ molecule. It has been reported that the major DR_{β} polymorphism revealed by serological (DR) or cellular (Dw) methods is encoded by the DR_BI gene and not by the DR_BIII gene (Gorski et al. 1987). Further, only a minority of all DR-restricted antigen-specific T-cell clones are indeed restricted by allelic products of $DR_{\beta}III$ (C. Irlé, personal communication). Finally, DRw52 and DRw53 molecules have been shown to be expressed at a four- to tenfold lower level than the classical DR molecules (Gregersen et al. 1986, Kratzin et al. 1986, Berdoz et al. 1987). Whether this also is the case for the DRw8/DRw52 molecule is not known. If so, it can be suggested that DR-restricted antigen presentation might be less efficient in DRw8 cells, since they express only a DR_BIII-related gene. Furthermore, it is well established that the repertoire of class II molecules on antigenpresenting cells influences the immune response (Benacerraf and Germain 1978, Zinkernagel and Doherty 1979), and it has been a common view that a broad class II repertoire is beneficial for the individual. If this latter assumption is correct, it would imply that individuals homozygous for DRw8, who only express a single variant of the DR₆ chain, should be at a disadvantage compared with individuals of other known DR genotypes who express two to four different variants of DR₆ chains. To the best of our knowledge there is no data indicating that this should be the case. However, DRw8 homozygotes must be very uncommon because of the fairly low haplotype frequency of DRw8.

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